

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10 | 815,320
Source: IFW O
Date Processed by STIC: 11 | 04 | 2005

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IFWO

RAW SEQUENCE LISTING

DATE: 11/04/2005

PATENT APPLICATION: US/10/815,320

TIME: 13:27:14

Input Set : N:\CrF3\RULE60\10815320.raw

Output Set: N:\CRF4\11042005\J815320.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Binz, Hans
6             Baussant, Thierry
7             Haeuw, Jean-Francois
8             Nguyen Ngoc, Thien
10    (ii) TITLE OF INVENTION: Carrier Protein Having an Adjuvant
11                                Effect, Immunogenic Complex Containing It, Process for
12                                Their Preparation, Nucleotide Sequence and Vaccines
14    (iii) NUMBER OF SEQUENCES: 8
16    (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
18            (B) STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
19                    4700
20            (C) CITY: Chicago
21            (D) STATE: Illinois
22            (E) COUNTRY: U.S.A.
23            (F) ZIP: 60601
25    (v) COMPUTER READABLE FORM:
26            (A) MEDIUM TYPE: Floppy disk
27            (B) COMPUTER: IBM PC compatible
28            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31    (vi) CURRENT APPLICATION DATA:
C--> 32            (A) APPLICATION NUMBER: US/10/815,320
C--> 33            (B) FILING DATE: 01-Apr-2004
W--> 39            (C) CLASSIFICATION: 424
36    (vii) PRIOR APPLICATION DATA:
37            (A) APPLICATION NUMBER: US/08/836,500
38            (B) FILING DATE: 11-Aug-1997
41    (viii) ATTORNEY/AGENT INFORMATION:
42            (A) NAME: Katz, Martin L.
43            (B) REGISTRATION NUMBER: 25,011
44            (C) REFERENCE/DOCKET NUMBER: PIE1514P0180US
46    (ix) TELECOMMUNICATION INFORMATION:
47            (A) TELEPHONE: 312-616-5400
48            (B) TELEFAX: 312-616-5460
51 (2) INFORMATION FOR SEQ ID NO: 1:
53     (i) SEQUENCE CHARACTERISTICS:
54            (A) LENGTH: 1007 base pairs
55            (B) TYPE: nucleic acid
56            (C) STRANDEDNESS: single
57            (D) TOPOLOGY: linear

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59      (ii) MOLECULE TYPE: cDNA
62      (ix) FEATURE:
63          (A) NAME/KEY: CDS
64          (B) LOCATION: 1..1007
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 GCT CCG AAA GAT AAC ACC TGG TAT GCA GGT GGT AAA CTG GGT TGG TCC      48
70 Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
71   1           5           10           15
73 CAG TAT CAC GAC ACC GGT TTC TAC GGT AAC GGT TTC CAG AAC AAC AAC      96
74 Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn
75           20           25           30
77 GGT CCG ACC CGT AAC GAT CAG CTT GGT GCT GGT GCG TTC GGT GGT TAC      144
78 Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr
79           35           40           45
81 CAG GTT AAC CCG TAC CTC GGT TTC GAA ATG GGT TAT GAC TGG CTG GGC      192
82 Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly
83   50           55           60
85 CGT ATG GCA TAT AAA GGC AGC GTT GAC AAC GGT GCT TTC AAA GCT CAG      240
86 Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln
87  65           70           75           80
89 GGC GTT CAG CTG ACC GCT AAA CTG GGT TAC CCG ATC ACT GAC GAT CTG      288
90 Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu
91           85           90           95
93 GAC ATC TAC ACC CGT CTG GGC GGC ATG GTT TGG CGC GCT GAC TCC AAA      336
94 Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys
95           100          105          110
97 GGC AAC TAC GCT TCT ACC GGC GTT TCC CGT AGC GAA CAC GAC ACT GGC      384
98 Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly
99           115          120          125
101 GTT TCC CCA GTA TTT GCT GGC GGC GTA GAG TGG GCT GTT ACT CGT GAC      432
102 Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp
103   130          135          140
105 ATC GCT ACC CGT CTG GAA TAC CAG TGG GTT AAC AAC ATC GGC GAC GCG      480
106 Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala
107 145          150          155          160
109 GGC ACT GTG GGT ACC CGT CCT GAT AAC GGC ATG CTG AGC CTG GGC GTT      528
110 Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val
111           165          170          175
113 TCC TAC CGC TTC GGT CAG GAA GAT GCT GCA CCG GTT GTT GCT CCG GCT      576
114 Ser Tyr Arg Phe Gly Gln Glu Asp Ala Ala Pro Val Val Ala Pro Ala
115           180          185          190
117 CCG GCT CCG GCT CCG GAA GTG GCT ACC AAG CAC TTC ACC CTG AAG TCT      624
118 Pro Ala Pro Ala Pro Glu Val Ala Thr Lys His Phe Thr Leu Lys Ser
119           195          200          205
121 GAC GTT CTG TTC AAC TTC AAC AAA GCT ACC CTG AAA CCG GAA GGT CAG      672
122 Asp Val Leu Phe Asn Phe Asn Lys Ala Thr Leu Lys Pro Glu Gly Gln
123           210          215          220
125 CAG GCT CTG GAT CAG CTG TAC ACT CAG CTG AGC AAC ATG GAT CCG AAA      720
126 Gln Ala Leu Asp Gln Leu Tyr Thr Gln Leu Ser Asn Met Asp Pro Lys

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127 225          230          235          240
129 GAC GGT TCC GCT GTT GTT CTG GGC TAC ACC GAC CGC ATC GGT TCC GAA      768
130 Asp Gly Ser Ala Val Val Leu Gly Tyr Thr Asp Arg Ile Gly Ser Glu
131          245          250          255
133 GCT TAC AAC CAG CAG CTG TCT GAG AAA CGT GCT CAG TCC GTT GTT GAC      816
134 Ala Tyr Asn Gln Gln Leu Ser Glu Lys Arg Ala Gln Ser Val Val Asp
135          260          265          270
137 TAC CTG GTT GCT AAA GGC ATC CCG GCT GGC AAA ATC TCC GCT CGC GGC      864
138 Tyr Leu Val Ala Lys Gly Ile Pro Ala Gly Lys Ile Ser Ala Arg Gly
139          275          280          285
141 ATG GGT GAA TCC AAC CCG GTT ACT GGC AAC ACC TGT GAC AAC GTG AAA      912
142 Met Gly Glu Ser Asn Pro Val Thr Gly Asn Thr Cys Asp Asn Val Lys
143          290          295          300
145 GCT CGC GCT GCC CTG ATC GAT TGC CTG GCT CCG GAT CGT CGT GTA GAG      960
146 Ala Arg Ala Ala Leu Ile Asp Cys Leu Ala Pro Asp Arg Arg Val Glu
147 305          310          315          320
149 ATC GAA GTT AAA GGC TAC AAA GAA GTT GTA ACT CAG CCG GCG GGT TA      1007
150 Ile Glu Val Lys Gly Tyr Lys Glu Val Val Thr Gln Pro Ala Gly
151          325          330          335
154 (2) INFORMATION FOR SEQ ID NO: 2:
156   (i) SEQUENCE CHARACTERISTICS:
157       (A) LENGTH: 335 amino acids
158       (B) TYPE: amino acid
159       (D) TOPOLOGY: linear
161   (ii) MOLECULE TYPE: protein
163   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
165 Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
166 1      5      10      15
168 Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn
169      20      25      30
171 Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr
172      35      40      45
174 Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly
175      50      55      60
177 Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln
178 65      70      75      80
180 Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu
181      85      90      95
183 Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys
184      100     105     110
186 Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly
187      115     120     125
189 Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp
190      130     135     140
192 Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala
193 145     150     155     160
195 Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val
196      165     170     175
198 Ser Tyr Arg Phe Gly Gln Glu Asp Ala Ala Pro Val Val Ala Pro Ala

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199          180          185          190
201 Pro Ala Pro Ala Pro Glu Val Ala Thr Lys His Phe Thr Leu Lys Ser
202          195          200          205
204 Asp Val Leu Phe Asn Phe Asn Lys Ala Thr Leu Lys Pro Glu Gly Gln
205          210          215          220
207 Gln Ala Leu Asp Gln Leu Tyr Thr Gln Leu Ser Asn Met Asp Pro Lys
208 225          230          235          240
210 Asp Gly Ser Ala Val Val Leu Gly Tyr Thr Asp Arg Ile Gly Ser Glu
211          245          250          255
213 Ala Tyr Asn Gln Gln Leu Ser Glu Lys Arg Ala Gln Ser Val Val Asp
214          260          265          270
216 Tyr Leu Val Ala Lys Gly Ile Pro Ala Gly Lys Ile Ser Ala Arg Gly
217          275          280          285
219 Met Gly Glu Ser Asn Pro Val Thr Gly Asn Thr Cys Asp Asn Val Lys
220          290          295          300
222 Ala Arg Ala Ala Leu Ile Asp Cys Leu Ala Pro Asp Arg Arg Val Glu
223 305          310          315          320
225 Ile Glu Val Lys Gly Tyr Lys Glu Val Val Thr Gln Pro Ala Gly
226          325          330          335
228 (2) INFORMATION FOR SEQ ID NO: 3:
230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 537 base pairs
232 (B) TYPE: nucleic acid
233 (C) STRANDEDNESS: single
234 (D) TOPOLOGY: linear
236 (ii) MOLECULE TYPE: cDNA
239 (ix) FEATURE:
240 (A) NAME/KEY: CDS
241 (B) LOCATION: 1..537
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
246 GCT CCG AAA GAT AAC ACC TGG TAT GCA GGT GGT AAA CTG GGT TGG TCC 48
247 Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
248 1 5 10 15
250 CAG TAT CAC GAC ACC GGT TTC TAC GGT AAC GGT TTC CAG AAC AAC AAC 96
251 Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn
252 20 25 30
254 GGT CCG ACC CGT AAC GAT CAG CTT GGT GCT GGT GCG TTC GGT GGT TAC 144
255 Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr
256 35 40 45
258 CAG GTT AAC CCG TAC CTC GGT TTC GAA ATG GGT TAT GAC TGG CTG GGC 192
259 Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly
260 50 55 60
262 CGT ATG GCA TAT AAA GGC AGC GTT GAC AAC GGT GCT TTC AAA GCT CAG 240
263 Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln
264 65 70 75 80
266 GGC GTT CAG CTG ACC GCT AAA CTG GGT TAC CCG ATC ACT GAC GAT CTG 288
267 Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu
268 85 90 95
270 GAC ATC TAC ACC CGT CTG GGC GGC ATG GTT TGG CGC GCT GAC TCC AAA 336

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271 Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys
272      100      105      110
274 GGC AAC TAC GCT TCT ACC GGC GTT TCC CGT AGC GAA CAC GAC ACT GGC      384
275 Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly
276      115      120      125
278 GTT TCC CCA GTA TTT GCT GGC GGC GTA GAG TGG GCT GTT ACT CGT GAC      432
279 Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp
280      130      135      140
282 ATC GCT ACC CGT CTG GAA TAC CAG TGG GTT AAC AAC ATC GGC GAC GCG      480
283 Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala
284 145      150      155      160
286 GGC ACT GTG GGT ACC CGT CCT GAT AAC GGC ATG CTG AGC CTG GGC GTT      528
287 Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val
288      165      170      175
290 TCC TAC CGC      537
291 Ser Tyr Arg
295 (2) INFORMATION FOR SEQ ID NO: 4:
297     (i) SEQUENCE CHARACTERISTICS:
298         (A) LENGTH: 179 amino acids
299         (B) TYPE: amino acid
300         (D) TOPOLOGY: linear
302     (ii) MOLECULE TYPE: protein
304     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
306 Ala Pro Lys Asp Asn Thr Trp Tyr Ala Gly Gly Lys Leu Gly Trp Ser
307  1      5      10      15
309 Gln Tyr His Asp Thr Gly Phe Tyr Gly Asn Gly Phe Gln Asn Asn Asn
310      20      25      30
312 Gly Pro Thr Arg Asn Asp Gln Leu Gly Ala Gly Ala Phe Gly Gly Tyr
313      35      40      45
315 Gln Val Asn Pro Tyr Leu Gly Phe Glu Met Gly Tyr Asp Trp Leu Gly
316      50      55      60
318 Arg Met Ala Tyr Lys Gly Ser Val Asp Asn Gly Ala Phe Lys Ala Gln
319  65      70      75      80
321 Gly Val Gln Leu Thr Ala Lys Leu Gly Tyr Pro Ile Thr Asp Asp Leu
322      85      90      95
324 Asp Ile Tyr Thr Arg Leu Gly Gly Met Val Trp Arg Ala Asp Ser Lys
325      100      105      110
327 Gly Asn Tyr Ala Ser Thr Gly Val Ser Arg Ser Glu His Asp Thr Gly
328      115      120      125
330 Val Ser Pro Val Phe Ala Gly Gly Val Glu Trp Ala Val Thr Arg Asp
331      130      135      140
333 Ile Ala Thr Arg Leu Glu Tyr Gln Trp Val Asn Asn Ile Gly Asp Ala
334 145      150      155      160
336 Gly Thr Val Gly Thr Arg Pro Asp Asn Gly Met Leu Ser Leu Gly Val
337      165      170      175
339 Ser Tyr Arg
342 (2) INFORMATION FOR SEQ ID NO: 5:
344     (i) SEQUENCE CHARACTERISTICS:
345         (A) LENGTH: 216 base pairs

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/815,320

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TIME: 13:27:15

Input Set : N:\Crf3\RULE60\10815320.raw

Output Set: N:\CRF4\11042005\J815320.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:39 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)